ACSIJ Advances in Computer Science: an International Journal, Vol. 3, Issue 5, No.11 , September 2014
ISSN : 2322-5157
www.ACSIJ.org

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A new centrality measure for probabilistic diffusion in network

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Abstract

Due to the significant increment of the volume of interactions among the population, probabilistic process on complex network can be often utilized to analyse diffusion phenomena in the society, then a number of researchers have studied especially from the perspectives of social network analysis, computer virus spread study, and epidemics study. So far, it has been believed that the largest eigenvalue and the principal eigenvector of the adjacency matrix can well approximate the dynamics on networks, but the accuracy of this approximation method has not study extensively. In our previous work, we found that not only the largest eigenvalue and the principle eigenvector but also the other eigenvalues and eigenvectors need to be considered when analysing the diffusion process on real networks. In this paper, we proposed a new centrality measure, the infection diffusion eigenvector centrality (IDEC), which considers all eigenvalues and eigenvectors. Our comparison results indicates that the IDEC shows better predictability than other centrality measures when the effective infection ratio is low, which will provide us with a good insight for practical application for developing the effective infection prevention methodology. Also, another interesting finding is that the eigenvector centrality shows poor predictability especially on the real networks. In addition, we conduct the recovery probability enforcement simulation, which highlights the advantage of IDEC for the range below the critical point.

Keywords: *Infection, SIS model, Complex network, Centrality, Eigenvalue, Eigenvector*

1. Introduction

Probabilistic diffusion analysis on complex network is being treated as having the potential applicability due to the well-connected modern society. Recently, the probabilistic diffusion models are often used to analyze the information spreads in the internet. Also, it has been often used to model and analyze the virus spread among the population. Recent concern from computer virus spread is also one of the applications which can be analysed by the probabilistic diffusion models.

In this paper, we utilize the Susceptible-Infected-Susceptible (SIS) model which is one of the typical probabilistic diffusion models and has been often used to analyse the infectious diseases and computer virus spread [1-6]. In the SIS model, every node in a network is probable to be put into two states (susceptible state and infected state). Then, the susceptible nodes are influenced from the infected-state neighbour nodes at a certain infection probability. At the same time, the infected nodes are probable to return to the susceptible state again at a certain recovery probability. Many researches have analysed and reported that the critical phenomena can be observed in the SIS model and, identifying the critical point have been getting significant attentions because it promote the efficiency of control the probabilistic diffusion dynamics [4,7-10]; for instance, it can help to propose the most cost effective vaccination strategy to prevent outbreaks of disease.

The first analysis of the SIS model for homogeneous network is conducted by Kephart and White [7]. Then, Wang et al. [8] analysed the SIS diffusion model from the spectral point of view. They propose that the critical point for any network can be approximated by the inverse of the largest eigenvalue of the adjacency matrix of the network. Mieghem et al. [9] established "the *N*-intertwined mean field approximation model" which provides with more accurate and rigorous analysis for the SIS model. In addition, Mieghem et al. [11] also rigorously analysed from spectral point of view, which also reported that the epidemic threshold can be approximately calculated by the inverse of the largest eigenvalue of the adjacency matrix of networks. However, in our previous work [12], based on the quantification of the accuracy of the approximation method utilizing only the largest eigenvalue of the adjacency matrix from the spectral point of view, we report that the accuracy is comparatively low in some real networks and not only the largest eigenvalue but also the other eigenvalues need to be considered on the real networks.

Centrality is a terminology that represents the relative importance of each node in a network. So far, a lot of definitions of the centrality metrics have been proposed [13]. Identifying the important nodes in a network is critical to control the diffusion dynamics occurring on the network and recently getting significant attention [e.g. 14]. In this paper, we propose a new centrality measure that is

derived from the analysis of the SIS diffusion model from spectral point of view. The proposed centrality measure, infection diffusion eigenvector centrality (IDEC), considers not only the largest eigenvalue and the principal eigenvector but also the non-largest eigenvalues and the corresponding eigenvectors. Then, IDEC shows better predictability to find the vulnerable node(s) for the SIS model in the real networks than that of the existing centrality measures, such as degree centrality, eigenvector centrality, and Alpha-centrality. In addition to that, we conduct the numerical simulation of the SIS diffusion model with enforcing the recovery probability being based on the significance of each centrality measures.

In the remaining of this paper, in the second section, we review some existing analytical frameworks. In the third section, we introduce our analytical frameworks from the spectral point of view. In the fourth section, we review the typical centrality measures. Then, the new centrality measure we propose is introduced in the fifth section and also the comparison results of predictability with the other centrality measures are discussed. In the sixth section, the recovery enforcement simulation results are reported. Finally, we conclude this paper in the seventh section.

2. Analytical Frameworks of Probabilistic Diffusion on Networks

2.1 Critical Point of the SIS Model

One of the important characteristics of the probabilistic diffusion on networks is the critical phenomenon. When investigating the evolution of the steady-state fraction of infected nodes, $y(\infty)$, as the function of the effective infection ratio, τ, which can be calculated by β/δ, we can observe that $y(\infty)$ suddenly begin to increase at a specific value of τ. Many researchers have been tried to identify the threshold, τ_c, and several approaches have been proposed to approximate the value of the critical point [7-10]. One of the most widely known results is that the threshold can be approximated by the inverse of the largest eigenvalue of the adjacency matrix as follows,

$$\tau_c = \frac{1}{\lambda_1(\mathbf{A})}, \tag{1}$$

where $\lambda_1(\mathbf{A})$ denotes the largest eigenvalue of the adjacency matrix **A**.

2.2 N-Intertwined Mean Field Approximation Model

The "N-intertwined mean field approximation" model, which is established by Mieghem et al. [9], results in the following Markov differential equation as matrix notation,

$$\begin{aligned}\frac{d\mathbf{V}(t)}{dt} &= \beta\mathbf{A}\mathbf{V}(t) - \mathrm{diag}\big(v_i(t)\big)(\beta\mathbf{A}\mathbf{V}(t) + \delta\mathbf{e}) \\ &= (\beta\mathbf{A} - \delta\boldsymbol{I})\mathbf{V}(t) - \beta\mathrm{diag}\big(v_i(t)\big)\mathbf{A}\mathbf{V}(t),\end{aligned} \tag{2}$$

where $v_i(t)$ denotes the probability that the node i is infected at time t, β is infection probability, δ is recovery probability, $\mathbf{V}(t) = \big(v_1(t), v_2(t), v_3(t), \cdots, v_N(t)\big)^T$, $\mathbf{e}$ is the all-one vector, and $\mathrm{diag}\big(v_i(t)\big)$ is the diagonal matrix in which the diagonal elements consist of $v_1(t), v_2(t), v_3(t), \cdots, v_N(t)$. According to the comparison results with the numerical simulation results in small networks, the accuracy of this model is good enough except the region around threshold.

3. Analysis from the Eigenvalue Point of View

When the fraction of infection on each node $v_i(t)$ is small, the second term can be ignored and the equation (2) can be solved using the eigenvalue decomposition,

$$\begin{aligned}\mathbf{V}(t) &= \mathbf{U}\mathrm{diag}(\exp((\beta\lambda_k - \delta))t)\mathbf{U}^{\mathrm{T}}\,\mathbf{V}(0) \\ &= \sum\nolimits_k \exp\big((\beta\lambda_k(\mathbf{A}) - \delta)t\big)\mathbf{u}_k\mathbf{u}_k^{\mathrm{T}}\,\mathbf{V}(0),\end{aligned} \tag{3}$$

where $\lambda_k(\mathbf{A})$ is kth eigenvalue of the adjacency matrix **A,** **U** denotes the orthonormal matrix in which the kth column consists of the eigenvector of the kth eigenvalue, and $\mathbf{u}_k$ is eigenvector of the kth eigenvalue of the adjacency matrix **A**. Assuming that the initial infection randomly occurs on each node i at the probability $v_i(0) = 1/N$, the probability of infection on the node i at time t can be obtained as below,

$$v_i(t) = \frac{1}{N}\sum_{k=1}^{N} \exp\big((\beta\boldsymbol{\lambda}_k - \delta)t\big)u_{ki}\|\mathbf{u}_k\|, \tag{4}$$

where the norm $\|\mathbf{u}_k\|$ stands for the sum of all elements of the eigenvector corresponding kth eigenvalue, that is $\|\mathbf{u}_k\| = u_{k1} + u_{k2} + u_{k3} + \cdots + u_{kn}$., and N denotes the number of nodes in the network. Furthermore, the fraction of infected nodes over the whole network $y(t)$ can be calculated by taking the average of $v_i(t)$ as follows,

$$\begin{aligned} y(t) &= \frac{1}{N}\sum_{i=1}^{N} v_i(t) \\ &= \frac{1}{N^2}\sum_{k=1}^{N} \exp\big((\beta\lambda_k - \delta)t\big)\|\mathbf{u}_k\|^2. \end{aligned} \tag{5}$$

In the previous literatures, accuracy of the approximation method only utilizing the largest eigenvalue have not been discussed extensively and considered that this approach is generally applicable for any network types. However, our analytical framework from the spectral point of view shows that not only the largest eigenvalue of the adjacency matrix but also the other non-largest eigenvalues is important to analyze diffusion processes more accurately, which was validated by numerical simulation [12]. Then our investigation of the real networks shows that the modular networks with high modularity tend to show the property that the influences from the non-largest eigenvalues and the corresponding eigenvectors are significant.

4. Centrality

Centrality is a terminology that represents the relative importance of each node in a network. So far, various types of centrality measures have been proposed in the scope of graph theory, social network analysis, and complex network study [e.g. 13].

Degree centrality (DC) is the one of the most widely used centrality measures and intuitively understandable. The definition of the DC is the number of links that the node connects to other nodes. When considering the directed networks, two degree centralities can be defined "in-degree centrality" and "out-degree centrality". The in-degree centrality is the number of links that come into the node, and the out-degree is the number of links that go out from the nodes. One of the famous facts relating to the degree centrality in complex networks is that the distribution of the number of each node shows the scale-free feature [1]. And, it is well known that this feature is observed in the artificially designed networks created by the preferential attachment network formation algorithm [1].

The eigenvector centrality (EVC) [15] is an index considering that a node connecting to influential nodes increases its influence. With respect to the DC, the DC only considers the influence from the surrounding nodes locating one-step away, but the EVC considers the effects from the other nodes in the entire network. Therefore, for the practical use, the EVC is believed to be more convenient to measure the relative influence of each node. However, the EVC is only usable for the mutually connecting and undirected network.

Controlling the properties of the nodes with high centrality is a possible and effective approach to control the dynamics on network because the nodes with high centrality are comparatively influential to the entire network. Recently, studies about the application of the centrality measures for controlling diffusion dynamics on networks are reported by many researchers (e.g. [14]). For instance, Alpha-centrality (AC) [16] is applied to control the SIS diffusion model in networks [17, 18]. The AC is defined as follows as a vector notation,

$$\mathbf{C}_{\alpha} = (\mathbf{I} - \alpha\mathbf{A})^{-1}\mathbf{e}, \tag{6}$$

where, α is an arbitrary parameter, **e** is an all-one vector, and **I** is a unit matrix.

In the SIS model, the infection probability vector, $\mathbf{p}(t)$, at time *t* can be represented as below,

$$\mathbf{p}(t) = \mathbf{M}^{t-1}\mathbf{p}(0), \tag{7}$$

where, $\mathbf{p}(0)$ denotes the initial infection probability and **M** denotes the transition probability matrix which can be calculated as below,

$$\mathbf{M} = (1-\delta)\mathbf{I} + \beta\mathbf{A}. \tag{8}$$

Then, utilizing by Tyler expansion, the accumulative infection probability on each node can be approximated with assuming infinite time as below,

$$\begin{aligned} \sum_{t=1}^{\infty}\mathbf{p}(t) = (\mathbf{I} + \mathbf{M} + \mathbf{M^2} + \mathbf{M^3} + \cdots + \mathbf{M}^t \\ + \cdots)\mathbf{p}(0) \approx (\mathbf{I} - \mathbf{M})^{-1}\mathbf{p}(0) \end{aligned} \tag{9}$$

Then, considering that the parameter α is the effective infection ratio β/δ, and assumes that the initial infections randomly occur, which means $\mathbf{p}(0) \propto \mathbf{e}$, the formula (9) can be formulated as follows,

$$\begin{aligned} (\mathbf{I} - \mathbf{M})^{-1}\mathbf{p}(0) &= \frac{1}{\delta}(\mathbf{I} - \alpha\mathbf{A})^{-1}\mathbf{p}(0) \\ &\propto (\mathbf{I} - \alpha\mathbf{A})^{-1}\mathbf{e} \equiv \mathbf{C}_{\alpha}. \end{aligned} \tag{10}$$

This analysis predicts that the Alpha-centrality on each node is proportional to the accumulative infection probability on each node.

In addition to that, an important analysis on the AC is that, when α become close to 0, the value of AC on each node is approximated to the DC as shown below,

$$\lim_{\alpha\to 0}(\mathbf{I}-\alpha\mathbf{A})^{-1}\mathbf{e} = \lim_{\alpha\to 0}(\mathbf{I} + \alpha\mathbf{A} + \alpha^2\mathbf{A}^2 + \alpha^3\mathbf{A}^3 + \cdots + \alpha^t\mathbf{A}^t + \cdots)\mathbf{e} \cong (\mathbf{I}+\alpha\mathbf{A})\mathbf{e}. \quad (11)$$

The physical significance of this analysis that, when the effective infection ratio is small (when $\alpha \cong 0$), the DC is a critical criterion when selecting the nodes to immune.
Furthermore, when α approaches to $1/\lambda_1(\mathbf{A})$ from below, the AC can be approximated to the EVC as can be derived as follows,

$$\begin{aligned}&\lim_{\alpha\to(1/\lambda_1(A))-}(\mathbf{I}-\alpha\mathbf{A})^{-1}\mathbf{e}\\ &= \lim_{\alpha\to(1/\lambda_1(A))-}\sum_{k=1}^{N}\frac{1}{1-\alpha\lambda_k}\mathbf{u}_k\mathbf{u}_k^T e \approx \mathbf{u}_1\mathbf{u}_1^T e\\ &= \left(\sum_{i=1}^{N}u_{k,i}\right)\mathbf{u}_1,\end{aligned} \quad (12)$$

where $\mathbf{u}_k$ denotes the eigenvector for the k^{th} eigenvalue and $u_{k,i}$ denotes the i^{th} element in the eigenvector $\mathbf{u}_k$. Because each element in the principal eigenvector, the EVC of each node corresponds to the elements of $\mathbf{u}_1$, the AC can be approximated to the EVC when $\alpha \cong 1/\lambda_1(\mathbf{A})$. The physical insights of this analysis that, when the effective infection ratio approach to the critical point, the EVC can be used to identify the influential nodes for effective mitigating.
However, if the effective infection ratio τ is larger than the critical point τ_c, the formula (9) diverges, which means that the AC cannot be applied to the regime over τ_c. Therefore, the normalized Alpha-centrality (NAC) measure is proposed [18], which can be applied to the whole regime of τ. The NAC for a given node n is calculated by dividing the AC on node n by the sum of the AC on every node as described below,

$$C_{NAC}(n) = \frac{C_{AC}(n)}{\sum_{i=1}^{N}C_{AC}(i)} \quad (13)$$

5. Infection Diffusion Eigenvalue Centrality

Based on the equation (4), we proposed a new centrality measure, the infection diffusion eigenvalue centrality (IDEC), which considers the influences from not only the largest eigenvalue and the principal eigenvector but also the other eigenvectors and eigenvalues. As we reported in our previous works [12], considering the non-largest eigenvalues and their corresponding eigenvectors is critical to analyse the diffusion dynamics in real networks, although the diffusion process has been approximately considered utilizing only the largest eigenvalue and the principal eigenvector.
The IDEC is defined as follows,

$$C_{IDE,i} \equiv \sum_{k=1}^{N}\exp(\beta\boldsymbol{\lambda}_k - \delta)u_{ki}\|\mathbf{u}_k\|, \quad (14)$$

where N denotes the number of nodes in the network, $u_{k,i}$ denotes the ith element of the eigenvector of the kth eigenvalue, and the norm $\|\mathbf{u}_k\|$ denotes the sum of all elements of the kth eigenvector.
To evaluate the performance of this new centrality measure, we compare the how the typical centrality measures (i.e. DC, EVC, NAC) and IDEC can predict the significance of infection on each node in the numerical simulation results. The numerical simulations consist of three processes as follows,

1) Conducting the SIS diffusion simulations on several networks.

2) Sorting the node-level simulation results (the number of infection on each node) as following the orders of significance of (i) the number of infection, (ii) DC, (iii) EVC, (iv) NAC, and (v) IDEC

3) Calculating Spearman's rank correlation coefficient between the sorted results of (i) and the results of (ii), (iii), (iv), and (v) respectively.

Table 1 shows the comparison results of the computed Spearman's rank correlation coefficient on 500-nodes Barabasi-Albert scale-free network (BA), 498-nodes Erdos-Renyi random network (RND), 500-nodes random regular network (RR), 379-nodes co-authorship network of network scientists (CNNS) [19, 20], and 419-nodes U.K. member of parliament Twitter network (UKMPTN) [21, 22]. The simulations ware done as changing the Score which is the effective infection ratio normalized by the simulated critical point, $\tau_{c,Sim}$, of each network. In each simulation, 10% of the nodes in each network are randomly chosen as the initial infected node. And, we repeated 100-time steps simulations 100 times with the same settings, then the outputs were averaged.
As can be seen in table 1, the proposed centrality, IDEC, shows better performance when the effective infection ratio is very small, which fit with the fact that we assume that the effective infection ratio is sufficiently small to obtain the equation (3). The insight which the IDEC is the best matrix for the small effective infection ratio provide with a good implication for effective infection prevention method because the individual targets to immune should be selected before outbreaks happen. Our simulation results for the other region of the effective infection ratio

show the NAC is the best choice to predict the vulnerable node on SIS model. Also, this comparison results indicate that the difference between independent network and modular network. RND and BA are the independent networks in which the entire network consists of only one network. On the contrary, the modular network in which the some densely connected sub networks sparsely interconnect each other, such as CNNS and UKPMTN, EVC shows poor predictability for all score, which means that we need to consider the all eigenvector and eigenvalues when we think the modular network that is the ubiquitous characteristics found in real networks.

Table 1: Comparisons of rank correlation coefficient between the simulation results ordered by the number of infection and the results ordered by the several centralities (DC, EVC, NAC, and IDEC).

Network	Centrality	Rank correlation coefficient for specific values of Score						
		0.5	0.6	0.7	0.8	0.9	1	2
RND N = 498	DC	0.3843	0.5110	0.6483	0.6942	0.8172	0.8500	0.9574
	EVC	0.3727	0.4706	0.6300	0.7204	0.8600	0.9352	0.9170
	NAC	0.3976	0.5171	0.6655	0.7397	0.8798	0.9325	0.9838
	IDEC	0.3990	0.5232	0.6661	0.7342	0.8660	0.9110	0.9954
BA N = 500	DC	0.1824	0.2770	0.2663	0.3187	0.3458	0.3480	0.4466
	EVC	0.3028	0.4111	0.5833	0.7159	0.8671	0.9428	0.8746
	NAC	0.2899	0.4149	0.5846	0.7125	0.8705	0.9359	0.8856
	IDEC	0.2883	0.4349	0.5858	0.7033	0.8600	0.9234	0.9244
CNNS N = 379	DC	0.4643	0.5156	0.6034	0.5976	0.6214	0.6209	0.7988
	EVC	0.2666	0.2144	0.3855	0.5373	0.5412	0.6524	0.3897
	NAC	0.4727	0.5394	0.6818	0.7780	0.8563	0.8450	0.9560
	IDEC	0.4795	0.5269	0.6525	0.6884	0.7500	0.7511	0.9467
UKMPTN N = 419	DC	0.3796	0.5015	0.5933	0.6458	0.6578	0.6124	0.8653
	EVC	0.3040	0.3411	0.4010	0.5654	0.6627	0.7313	0.5455
	NAC	0.3669	0.5484	0.6785	0.7861	0.8506	0.8539	0.9663
	IDEC	0.3828	0.5468	0.6676	0.7581	0.8011	0.7929	0.9877

6. Enhancement of Network Resilience using Centrality Measurement

In this section, we show the simulation results when the recovery probability of each node is proportional to the significance of its centrality. In the real world context, there are some situations that can be considered that this recovery probability enforcement is suitably applicable, such as the improvement of the recovery probability against a specific disease, or restraining the rumor spread by the information control, and so on. The enforced recovery probability of each node is determined by the following rules.

1) For a specific centrality measure, calculate the centrality in the all networks and finding a network that shows the highest centrality value.

2) Dividing the centrality values on each node in the network identified in the step 1 by the largest centrality value. Then, computing the sum of the centrality of the network.

3) The sum of the recovery probability in the step 2 is distributed as following the relative significance of each centrality measure.

4) The infection probability, β, for all nodes is determined by multiplying the average value of the recovery probability determined in the step 3 and the effective infection ratio.

5) Conducting the SIS diffusion simulation and calculating the averaged integrated number of infection until 100 time-steps, which is defined as the accumulative infection number, A, in the following formula, then comparing the integrated values to evaluating which centrality-based recovery enforcement strategy can reduce the number of infection, which can measure the performance of the centrality measures,

$$A \equiv \sum_{t=0}^{100} n(t), \tag{15}$$

where where $n(t)$ denotes the number of infected nodes over the whole network.

Figure 1 shows the comparison results of the four recovery enforcement strategies on the two independent networks (RND and BA) and the two real-world modular networks (CNNS and UKMPTN). As indicated in this figure, for the all four networks, the recovery probability enforcement strategy based on IDEC shows the best performance

when τ is comparatively small. In addition, the recovery probability enforcement strategy based on the eigenvector centrality does not demonstrate effective reduction of infections, especially in real networks, which support our expectation that only considering the largest eigenvalue and the principal eigenvalue is not sufficient to analyse the dynamics on real networks, and we need to consider the non-largest eigenvalues and the corresponding eigenvectors.

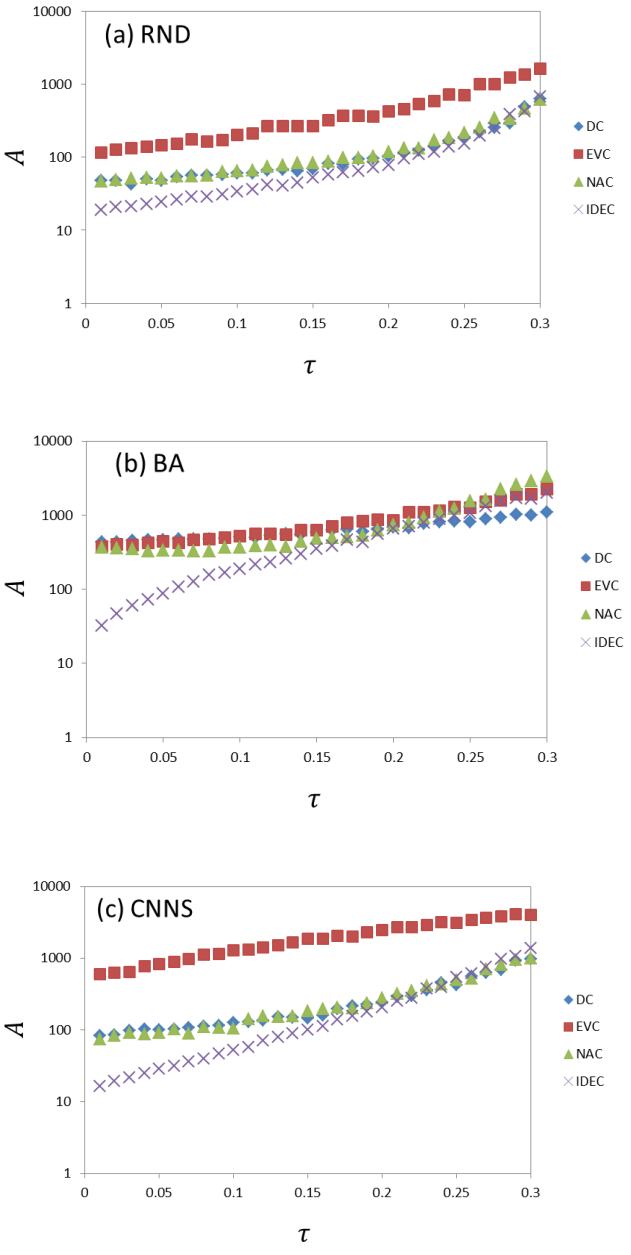

Fig. 1 The comparison of the centrality-based recovery probability enforcement strategy, (a) for 500-nodes random network (RND), (b) for 500-nodes Barabasi-Albert scale-free network (BA), (c) 379-nodes Co-author network of network scientists (CNNS), and (d) 419-nodes U.K. member of parliament on Twitter network (UKMPTN). Each plot represents the value of the accumulative infection number (AIN, A) which denotes the accumulative number of infection until 100 time-steps over the network for the four networks as the function of effective infection ratio τ.

7. Conclusions

In this paper, we proposed a new centrality measure, infection diffusion eigenvector centrality (IDEC), which derived from the analysis of the SIS model on networks from spectral point of view. IDEC considers all eigenvalues and corresponding eigenvectors, even though the previous analysis of the SIS diffusion model from the spectral point of view often considers only the largest eigenvalue and the principal eigenvector can approximate the property of the SIS diffusion dynamics. Then, our comparisons examination results that the IDEC shows high predictability when the effective infection ratio is below the critical point, which is the expected from the analytical framework. Also, we compared the simulation results when the recovery probability of each node increases as following the significance of each centrality measure. This recovery probability enforcement examination results that the recovery probability enforcement strategy using the IDEC is better to refrain the infection when the effective infection ration is comparatively small. In addition to that, one prominent insight of this work is that the eigenvector centrality poorly performs especially on the real networks, which is because, when analyzing the real networks, we must consider the effects from the non-largest eigenvalues and the corresponding eigenvectors as we precisely analyze in our previous work [12].

As our future works, we will develop an analytical framework from the spectral point of view for SIR and SIRS model. Also, for more realistic scenarios on epidemic spread, we will use the dynamically changing human contact network.

Acknowledgments

The authors would like to thank anonymous reviewers for their valuable comments. This research is supported in part by Grant-in-Aide for Scientific Research in Japan No.25330277 & No.26282089.

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